

## FIG. 1A

|   |     |     |     |
|---|-----|-----|-----|
| GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT  |     |     | 54  |
| Met Leu Ser Thr Ser   |     |     |     |
| 1   |     | 5   |     |
| CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC |     |     | 102 |
| Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr |     |     |     |
| 10  |     | 15  | 20  |
| ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG |     |     | 150 |
| Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val |     |     |     |
| 25  | 30  | 35  |     |
| AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC |     |     | 198 |
| Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe |     |     |     |
| 40  | 45  | 50  |     |
| ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC |     |     | 246 |
| Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn |     |     |     |
| 55  | 60  | 65  |     |
| TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC |     |     | 294 |
| Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala |     |     |     |
| 70  | 75  | 80  | 85  |
| ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT |     |     | 342 |
| Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser |     |     |     |
| 90  | 95  | 100 |     |
| GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA |     |     | 390 |
| Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr |     |     |     |
| 105   | 110 | 115 |     |
| GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC |     |     | 438 |
| Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu |     |     |     |
| 120   | 125 | 130 |     |
| CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA |     |     | 486 |
| Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu |     |     |     |
| 135   | 140 | 145 |     |

## FIG. 1B

|   |     |     |     |
|---|-----|-----|-----|
| AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC ACC TGG |     |     | 534 |
| Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp     |     |     |     |
| 150   | 155 | 160 | 165 |
| TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC     |     |     | 582 |
| Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys     |     |     |     |
| 170   | 175 | 180 |     |
| CAG AAA GAA GAT TCT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA         |     |     | 630 |
| Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly     |     |     |     |
| 185   | 190 | 195 |     |
| TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG     |     |     | 678 |
| Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu     |     |     |     |
| 200   | 205 | 210 |     |
| CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG     |     |     | 726 |
| Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu     |     |     |     |
| 215   | 220 | 225 |     |
| CTT CGG TGT CGA AAC GAG AAG AGG CAT AGG GCA GTG AGA GTC ATC         |     |     | 774 |
| Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile     |     |     |     |
| 230   | 235 | 240 | 245 |
| TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT     |     |     | 822 |
| Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile     |     |     |     |
| 250   | 255 | 260 |     |
| GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT     |     |     | 870 |
| Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys     |     |     |     |
| 265   | 270 | 275 |     |
| GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT     |     |     | 918 |
| Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu     |     |     |     |
| 280   | 285 | 290 |     |
| GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG     |     |     | 966 |
| Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly     |     |     |     |
| 295   | 300 | 305 |     |

## FIG. 1C

|   |      |
|---|------|
| GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC       | 1014 |
| Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala       |      |
| 310                   315                   320                   325 |      |
| CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG       | 1062 |
| Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys       |      |
| 330                   335                   340                       |      |
| AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA       | 1110 |
| Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly       |      |
| 345                   350                   355                       |      |
| AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA       | 1158 |
| Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly       |      |
| 360                   365                   370                       |      |
| GCC TAGAGACAGA AATGACAGAT CTCTGCTTG GAAATCACAC GTCTGGCTTC             | 1121 |
| Ala   |      |
| ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAAGGAG GAAGGCTGAG      | 1271 |
| AGGAGAGAGA CTCCAGCTGG GTTGGAAAAC AGTATTTCC AAACCTACCTT CCAGTTCCCTC    | 1331 |
| ATTTTGAAAT ACAGGCATAG AGTTCAGACT TTTTTAAAT AGTAAAATA AAATTAAAGC       | 1391 |
| TGAAAACCTGC AACTGTAAA TGTGGTAAAG AGTTAGTTG AGTTGCTATC ATGTCAAACG      | 1451 |
| TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTG AGCTTAAGAA TTTTGAGCAG      | 1511 |
| GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA     | 1571 |
| GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCGATGCAGC ATCTAAGTAA TGATGTCGTT    | 1631 |
| TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTG TCTCAGGCTT     | 1691 |
| GCTGCCAAAA GCCTTTGTG TTTGTTTG TATCATTATG AAGTCATGCG TTTAATCACA        | 1751 |
| TTCGAGTGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTGCCA    | 1811 |
| GTGGGAACTC CTAAATCAA TTGGCTTCTA ATCAAAGCTT TTAAACCCCTA TTGGTAAAGA     | 1871 |

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## FIG. 1D

|   |      |
|---|------|
| ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT   | 1931 |
| AAGAACATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC | 1991 |
| TTCTAGAACCG AGGCAACTTG GGAACTAGAC TCCCAAGCTG GACTATGGCT CTACTTCAG   | 2051 |
| GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA   | 2111 |
| TATATTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA    | 2171 |
| TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA   | 2231 |
| G   | 2232 |

## FIG. 2A

CAGGACTGCC TGAGACAAGC ACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT 60  
 TTCCCCAGTA CATCCACAAAC ATG <sup>84</sup>CTG TCC ACA TCT CGT TCT CGG TTT ATC 110  
 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile  
 1 5 10  
<sup>\*33</sup>  
 AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT 158  
 Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr  
 15 20 25  
 GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC 206  
 Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala  
 30 35 40  
 CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG 254  
 Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val  
 45 50 55  
 GGC AAC ATG CTG GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG 302  
 Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys  
 60 65 70  
 TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT 350  
 Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu  
 75 80 85 90  
 TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG 398  
 Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp  
 95 100 105  
 GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC 446  
 Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile  
 110 115 120  
 GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA 494  
 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg  
 125 130 135  
 TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC 542  
 Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val  
 140 145 150

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## FIG. 2B

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|   |     |      |     |
|---|-----|------|-----|
| ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT |     | 590  |     |
| Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe |     |      |     |
| 155   | 160 | 165  | 170 |
| GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT |     | 638  |     |
| Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser |     |      |     |
| 175   | 180 | 185  |     |
| GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC |     | 686  |     |
| Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His |     |      |     |
| 190   | 195 | 200  |     |
| ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG |     | 734  |     |
| Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met |     |      |     |
| 205   | 210 | 215  |     |
| GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC |     | 782  |     |
| Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn |     |      |     |
| 220   | 225 | 230  |     |
| GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT |     | 830  |     |
| Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile |     |      |     |
| 235   | 240 | 245  | 250 |
| GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC |     | 878  |     |
| Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn |     |      |     |
| 255   | 260 | 265  |     |
| ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA |     | 926  |     |
| Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln |     |      |     |
| 270   | 275 | 280  |     |
| CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC |     | 974  |     |
| Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys |     |      |     |
| 285   | 290 | 295  |     |
| TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG |     | 1022 |     |
| Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg |     |      |     |
| 300   | 305 | 310  |     |

FIG. 2C

|   |     |      |
|---|-----|------|
| TAT CTC TCG GTG TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA       |     | 1070 |
| Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys   |     |      |
| 315   | 320 | 325  |
| 330   |     |      |
| CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA   |     | 1118 |
| Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr   |     |      |
| 335   | 340 | 345  |
| AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA           |     | 1160 |
| Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu           |     |      |
| 350   | 355 | 360  |
| TAAAACGAGG AGCAGTTGA TTGTTGTTA TAAAGGGAGA TAACAATCTG TATATAACAA   |     | 1220 |
| CAAACCTCAA GGGTTGTTG ACAATAGAA ACCTGTAAAG CAGGTGCCA GGAACCTCAG    |     | 1280 |
| GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA |     | 1340 |
| TAATCCAGAA AAACGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG  |     | 1400 |
| AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTCTAG TCTTCATAAT TTCTTCACTC  |     | 1460 |
| AATCTCTGAT TCTGTCAATG TCTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG  |     | 1520 |
| TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGTC AGGGCTGAGA GGAGAAGGAG  |     | 1580 |
| GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT |     | 1640 |
| CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTAA CCTTGAAGGG  |     | 1700 |
| TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTGG TGGAGTCCGA  |     | 1760 |
| TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGCTTT ATTACAGTTT ATCTATGGCA  |     | 1820 |
| CCCATGCACC TTACATTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT  |     | 1880 |
| AGGCCACATC CCCCTGTCTA AAAATTAGA AAATTTTGT TTATAAAAGA TGCATTATCT   |     | 1940 |
| ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG                        |     | 1979 |

FIG. 3(A)

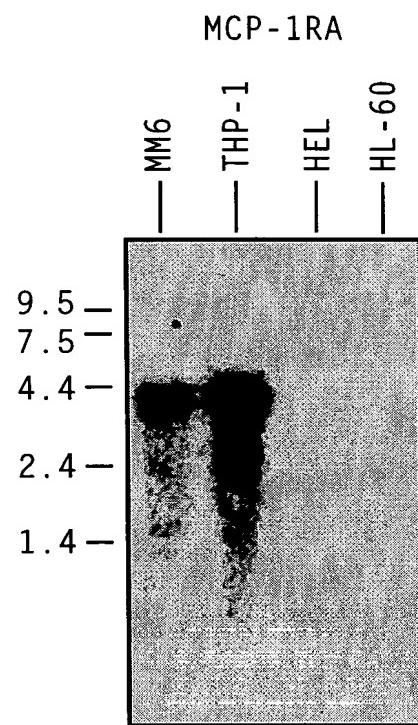


FIG. 3(B)

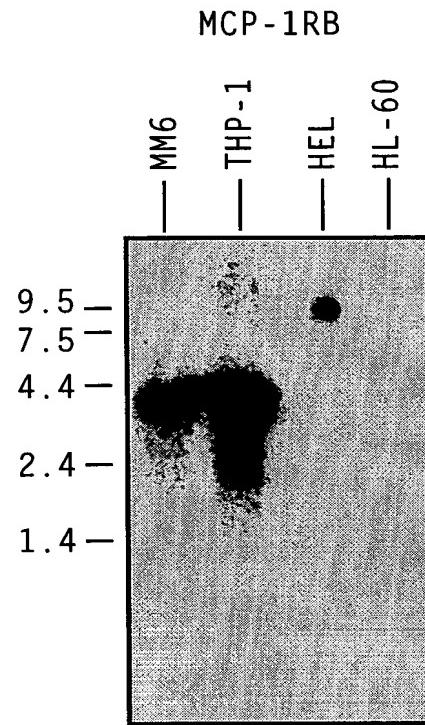


FIG.4(A)

|                         |  |     |
|-------------------------|--|-----|
| MCP-1RA (CCR2-A)        | MLSTSRSRFIRNTNESGEEVTTIFFDYDYG--APCHKFDVKQIGAQLLPPL      | 48  |
| MIP-1 $\alpha$ /RANTESR | M-----ETPNTEDYDTITTEFDYGDATPCQKVNERAFGAQLLPPL            | 40  |
| HUMSTSR                 | MEGIS---IYTSDNYTEEMGS-GDYDSMK-EPCFREENANFNKIFLPTI        | 44  |
| IL-8RA                  | MSNITDPQ-MWDFDDLNFTGMPPADEDY---SPC-MLETETLNKYVIIA        | 45  |
| IL-8RB                  | MESDSFEDFWKGEDLSNYSYSSTLPPFLDAAPC-EPESLEINKYFVII         | 49  |
|                         | 48            1            69            79            2 |     |
| MCP-1RA (CCR2-A)        | YSLVFIFGFVGMLVVLLILINCKKLKCLTDIYLLNL AISDLLFLITLPLW      | 98  |
| MIP-1 $\alpha$ /RANTESR | YSLVFVIGLVGNILVVLLVLVQYKRLKNMTSIIYLLNL AISDLLFLITLPLW    | 90  |
| HUMSTSR                 | YSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRHLHSVADLLFVITLPLW       | 94  |
| IL-8RA                  | YALVFLSLLGNSLVMILVILYSRVGRSVTDVYLLNLALADLLFALTLPWIW      | 95  |
| IL-8RB                  | YALVFLSLLGNSLVMILVILYSRVGRSVTDVYLLNLALADLLFALTLPWIW      | 99  |
|                         | 101            115            3            136           |     |
| MCP-1RA (CCR2-A)        | AH-SAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVF       | 147 |
| MIP-1 $\alpha$ /RANTESR | IDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFIILLTIDRYLAIVHAVF       | 140 |
| HUMSTSR                 | AV-DAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRLAIVHATN        | 143 |
| IL-8RA                  | AA-SKVNGWIFGTFLCKVVSSLKEVNFYSGILLACISVDRYLAIVHATR        | 144 |
| IL-8RB                  | AA-SKVNGWIFGTFLCKVVSSLKEVNFYSGILLACISVDRYLAIVHATR        | 148 |
|                         | 154            4            178                          |     |
| MCP-1RA (CCR2-A)        | ALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP--       | 195 |
| MIP-1 $\alpha$ /RANTESR | ALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTCSLHFPE        | 190 |
| HUMSTSR                 | SQRPRKLLAEKVVYVGWIPALLTIPDFIFANVSEADDRYICDRFYPN-         | 192 |
| IL-8RA                  | TLTQKR-HLVKFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEVLG        | 193 |
| IL-8RB                  | TLTQKRYLVKFI-CLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDMGN       | 197 |
|                         | 204            5            231                          |     |
| MCP-1RA (CCR2-A)        | --RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVR       | 243 |
| MIP-1 $\alpha$ /RANTESR | SLREWKLHQALKLNLFGLVLPLLVMICYTGIIKILLRRPNEKKS-KAVR        | 239 |
| HUMSTSR                 | --DLWVVVFQFQHIMVGLILPGIVILFCYCIIISKLSHSKGHQKR-KALK       | 239 |
| IL-8RA                  | DTAKWRMVLRLILPHTFGFIVPLFVMLFCYGFTLRTLFAHMGQK-HRAMR       | 242 |
| IL-8RB                  | NTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFAHMGQ-KHRAMR        | 246 |
|                         | 244            6            268                          |     |
| MCP-1RA (CCR2-A)        | VIIFTIMIVYFLFWTPYNIVILLNTFQEFGGLSNCESTSQLDQATQVTET       | 292 |
| MIP-1 $\alpha$ /RANTESR | LIFVIMIIFFLFWTPYNLTILISVFQDF-LFTHECEQSRHLDLAVQVTEV       | 288 |
| HUMSTSR                 | TTVILILAFFACWLPPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEA      | 289 |
| IL-8RA                  | VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNNIGRALDATEI       | 292 |
| IL-8RB                  | VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI       | 296 |

FIG. 4(B)

|                         | 295  | 7 | 313 |            |
|-------------------------|--|---|-----|------------|
| MCP-1RA (CCR2-A)        | LGMTHCCINPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKN | * |     | 342        |
| MIP-1 $\alpha$ /RANTESR | IAYTHCCVNPNVIYAFVGERFRKYLRQLFHRRA                  |   |     | VHLVKW 327 |
| HUMSTSR                 | LAFFHCCLNPIIYAFLGAKFKTSAQHALTS                     |   |     | VSRGSS 325 |
| IL-8RA                  | LGFLHSCLNPIIYAFIGQNFRHGFLKILA                      |   |     | MHGLVS 327 |
| IL-8RB                  | LGILHSCLNPLIYAFIGQKFRHGLLKILAIH                    |   |     | GLIS 331   |
|                         |  |   |     |            |
| MCP-1RA (CCR2-A)        | VKVTTQGLLDGRGKGKSIGRAPEASLQDKEGA                   |   |     | 374        |
| MIP-1 $\alpha$ /RANTESR | LPFLSVDRLE-RVSSTS-PSTGEHEL-SAGF                    |   |     | 355        |
| HUMSTSR                 | LKILSKGK---RGGHSSVSTESESSS--FHSS                   |   |     | 352        |
| IL-8RA                  | KEFLARH---RVTSYT-SSSVNVS---SNL                     |   |     | 350        |
| IL-8RB                  | KDSLPKDS---RPSFVG-SSSGHTS---TTL                    |   |     | 355        |

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FIG. 5

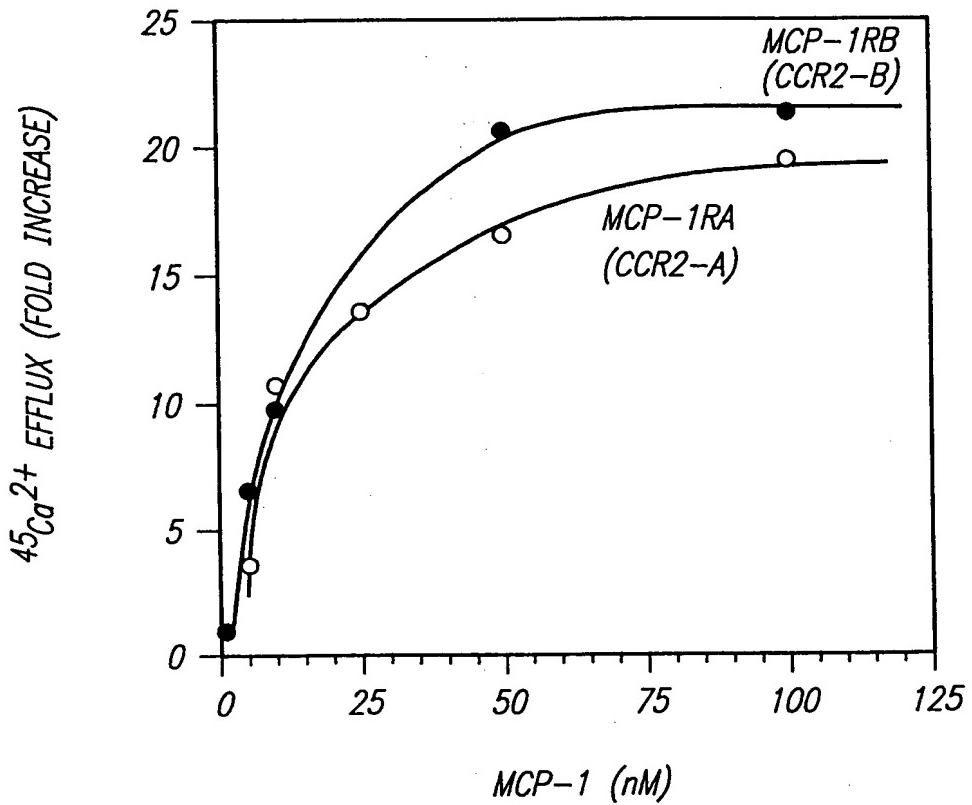
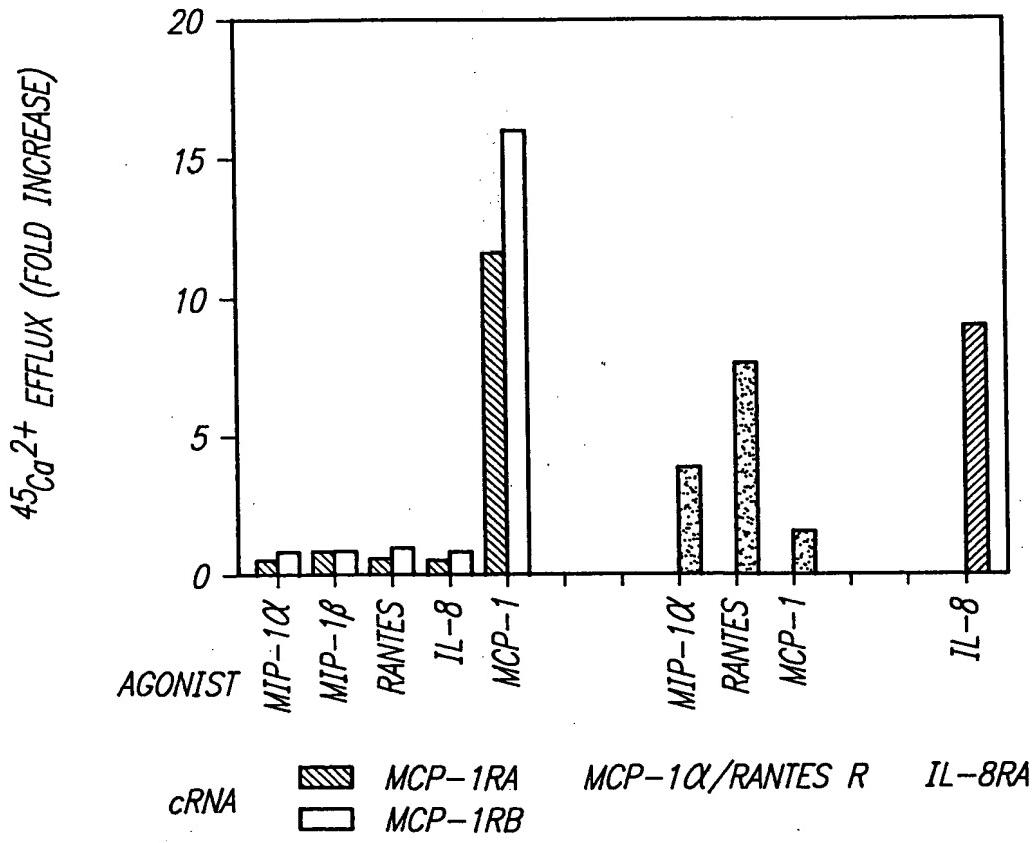


FIG. 6



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FIG. 7A MCP-1 RB

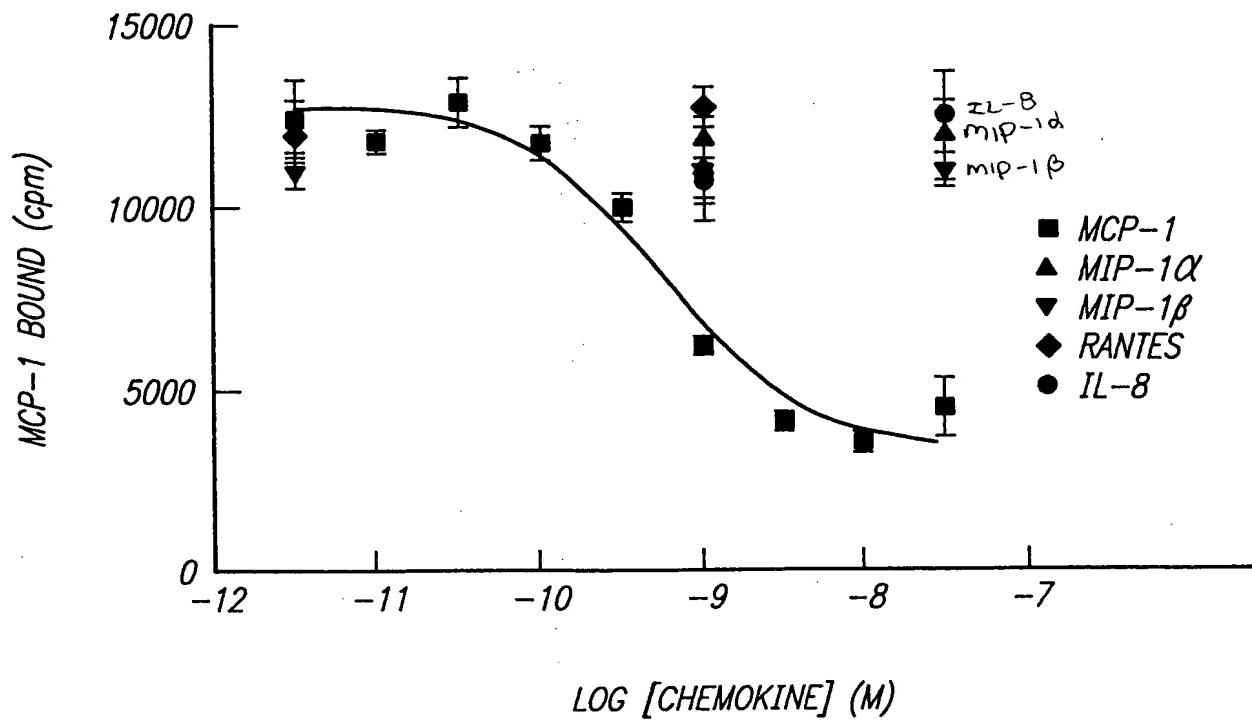
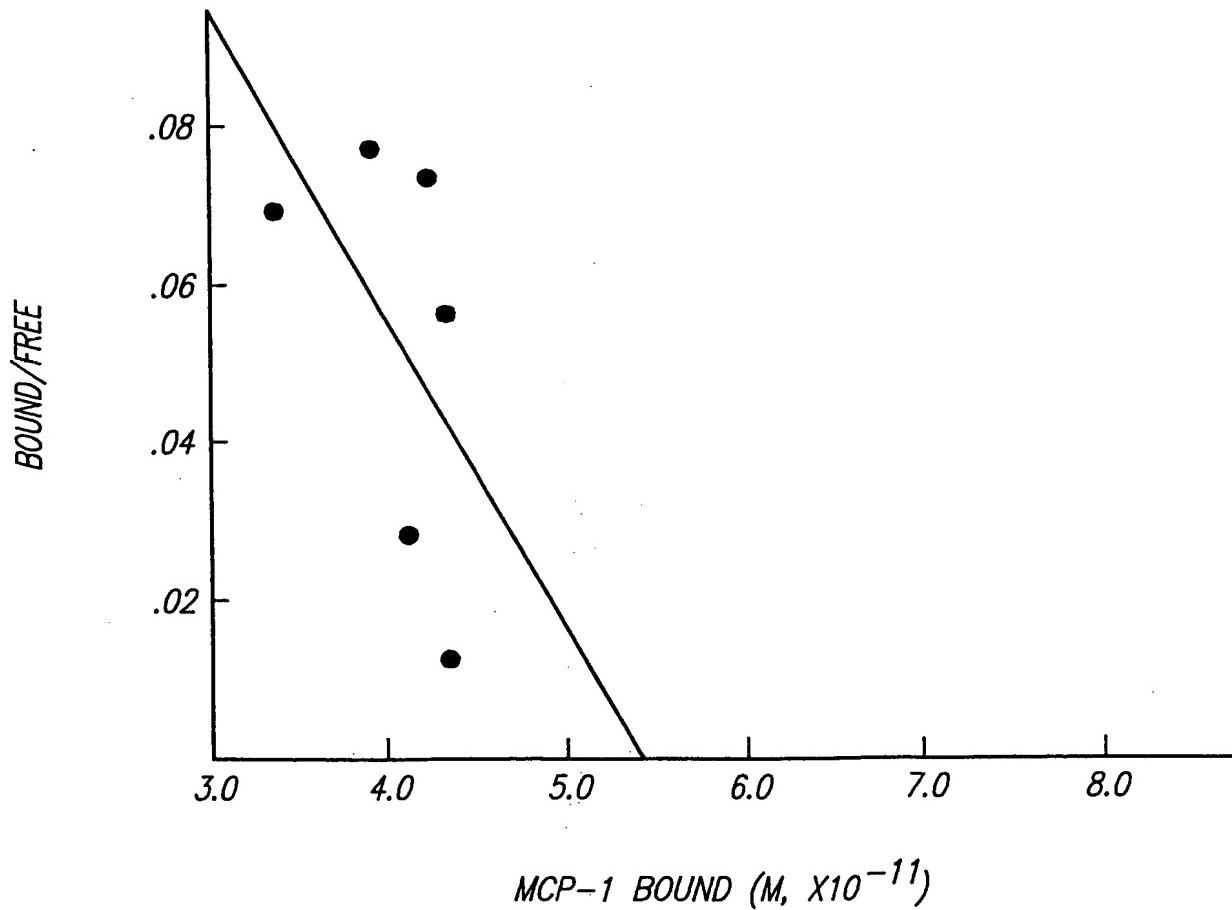
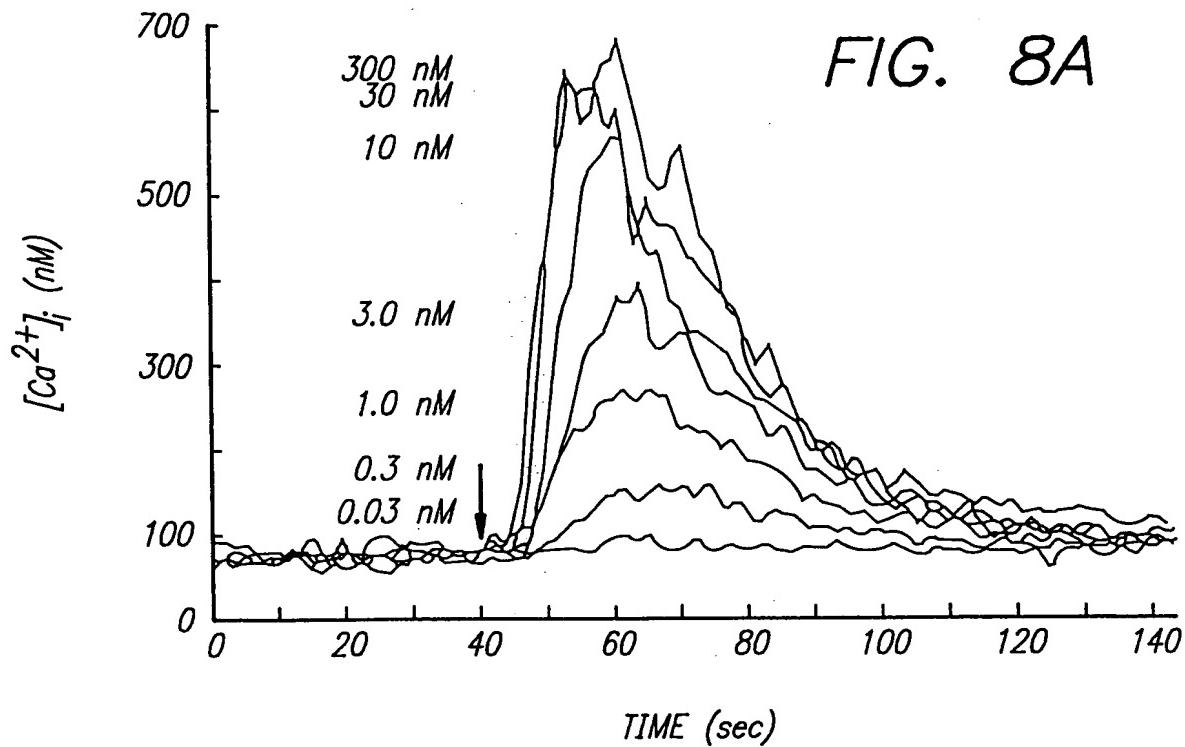
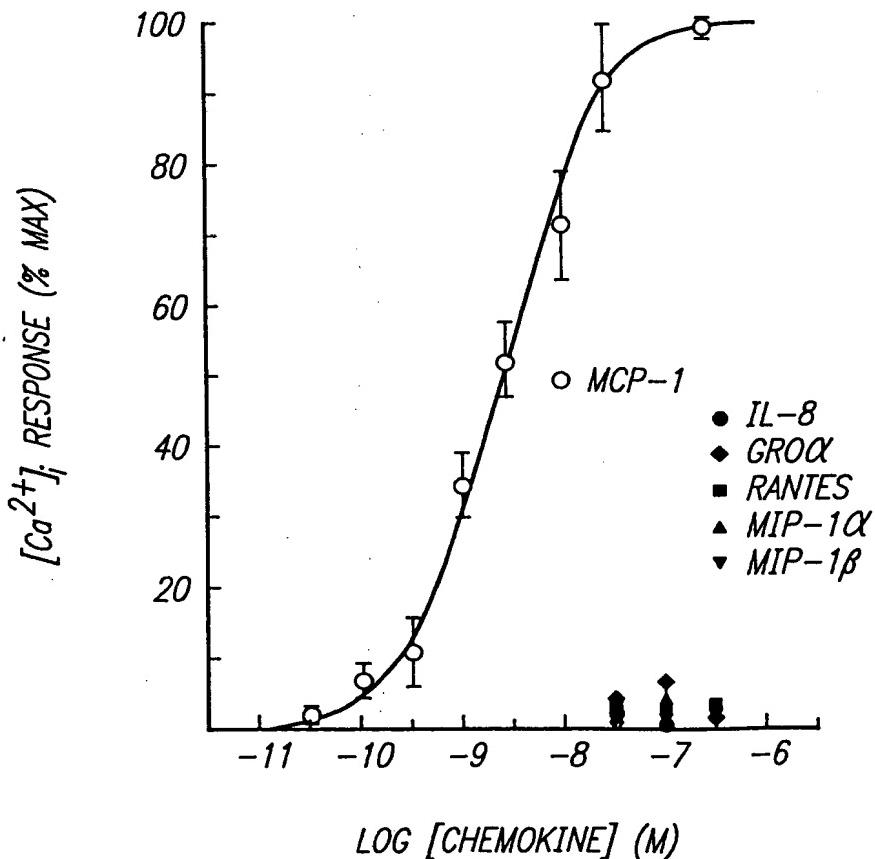


FIG. 7B



**FIG. 8B**

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FIG. 8C

